SEQUENCE LISTING

<110> KIM, Young Tae
LEE, Jae Hyung

<120> Gene involved in the biosynthesis of carotenoid and marine microorganism, paracoccus haeundaesis, producing the carotenoid

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<140> US 10/551,508
<141> 2006-06-05

<150> PCT/KR2004/000752
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Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Phe Ile Ala
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His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Gly Asn
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Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
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Arg Lys Met Ile Val Lys His Met Ala His His Arg His Thr Gly Thr
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Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
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Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro

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Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
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Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
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Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
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Gly Trp His Lys Ser His His Glu Glu His Asp His Ala Leu Glu Lys
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Met Thr Val Tyr Gly Leu Ile Tyr Phe Val Leu His Asp Gly Leu Val
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His Cys Val Ser Phe Gly Phe Ile Tyr Ala Pro Pro Val Asp Lys Leu
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Asp Pro Asp Leu Ser Pro His Trp Leu Ala Arg Leu Lys Pro Leu Arg
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Arg Ala Asn Trp Pro Asp Gln Glu Val Arg Phe Pro Arg His Ala Arg
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Arg Leu Ala Thr Gly Tyr Gly Ser Leu Asp Gly Ala Ala Leu Ala Asp
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Ala Val Ala Arg Ser Gly Ala Glu Ile Arg Trp Asn Ser Asp Ile Ala
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Leu Leu Asp Glu Gln Gly Ala Thr Leu Ser Cys Gly Thr Arg Ile Glu
115 120 125

Ala Gly Ala Val Leu Asp Gly Arg Gly Ala Gln Pro Ser Arg His Leu
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Thr Val Gly Phe Gln Lys Phe Val Gly Val Glu Ile Glu Thr Asp Cys
145 150 155 160

Pro His Gly Val Pro Arg Pro Met Ile Met Asp Ala Thr Val Thr Gln
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Gln Asp Gly Tyr Arg Phe Ile Tyr Leu Leu Pro Phe Ser Pro Thr Arg
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Ile Leu Ile Glu Asp Thr Arg Tyr Ser Asp Gly Gly Asn Leu Asp Asp
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Pro Val Gly Leu Arg Ala Gly Phe Phe His Pro Val Thr Gly Tyr Ser
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Pro Pro Gly Thr Asp Ala Leu Arg Gly Ala Ile Arg Asp Tyr Ala Ile
290 295 300

Asp Arg Ala Arg Arg Asp Arg Phe Leu Arg Leu Leu Asn Arg Met Leu
305 310 315 320

Phe Arg Gly Cys Ala Pro Asp Arg Arg Tyr Thr Leu Leu Gln Arg Phe
325 330 335

Tyr Arg Met Pro His Gly Leu Ile Glu Arg Phe Tyr Ala Gly Arg Leu
340 345 350

Ser Val Ala Asp Gln Leu Arg Ile Val Thr Gly Lys Pro Pro Ile Pro
355 360 365

Leu Gly Thr Ala Ile Arg Cys Leu Pro Glu Arg Pro Leu Leu Lys Glu
370 375 380

Asn Ala
385

<210> 11
<211> 1506
<212> DNA
<213> Paracoccus haeundaesis

<220>
<223> crtI gene

<400> 11
atgaacgccc attcgcccgc ggccaagacc gccatcgtga tcggcgcagg ctttggcggg 60

ctggccctgg ccatccgcct gcagtccgcg ggcatcgcca ccaccctggt cgaggcccgg 120

gacaagcccg gcgggcgcgc ctatgtctgg cacgatcagg gccatgtctt cgacgcgggc 180

ccgaccgtca tcaccgaccc cgatgcgctc aaggagctgt gggcgctgac cgggcaggac 240

atggcgcgcg acgtgacgct gatgccggtg tcgcccttct atcgactgat gtggccgggc 300

gggaaggtct tcgattacgt gaacgaggcc gatcagctgg agcgccagat cgcccagttc 360

aacccggacg acctggaagg ataccgccgc ttccgtgatt acgcggagga ggtgtatcag 420

gagggctacg tcaagctggg caccgtgccc ttcctcaagc tgggccagat gctcaaggcc 480

gcgcccgcgc tgatgaagct ggaggcctat aagtccgtcc atgccaaggt cgcgaccttc 540

atcaaggacc cctatctgcg gcaggcgttt tcgtatcaca cgctgctggt gggcgggaat 600

cccttctcga ccagctcgat ctatgcgctg atccacgcgc tggagcggcg cggcggggtc 660

tggttcgcca agggcggcac caaccagctg gtcgcgggca tggtcgcgct gttcgaacgg 720

cttggcggcc agatgatgct gaacgccaag gtcgcccgga tcgagaccga gggcgcgcgg 780

accacgggcg tcaccctggc ggacgggcgg tctttaaggg ccgacatggt cgccagcaac 840

ggcgacgtca tgcacaacta tcgcgacctg ctgggccaca cggcccgcgg gcagagccgc 900

gcgaaatcgc tggaccgcaa gcgctggtcc atgtcgttgt tcgtgctgca tttcggtctg 960

cgcgaggcgc ccaaggacat cgcgcatcac accatcctgt tcggcccccg ctacagggag 1020

ctggtcaacg agatcttcaa gggcccgaag ctggccgagg atttctcgct gtacctgcat 1080

tcgccctgca cgaccgatcc ggacatggcg cctccgggca tgtccacgca ttacgtgctg 1140

gcccccgtgc cgcatctggg ccgcgccgag atcgattggg cggtcgaggg gccgcgctat 1200

gccgaccgca tcctggcgtc cctggaggag cggctgatcc cgaacctgcg cgccaacctg 1260

accacgacgc gcatcttcac gcccgccgat ttcgccagcg aactgaacgc ccatcacggc 1320

agcgccttct cggtcgagcc gatcctgacg caatccgcgt ggttccggcc gcacaaccgc 1380

gacaagacga tccgcaactt ctatctggtc ggcgcgggca cccatccggg cgcgggcatt 1440

ccgggcgtcg tgggctcggc caaggccacg gcccaggtga tgctgtccga cctggcgggc 1500

gcatga 1506

<210> 12
<211> 501
<212> PRT
<213> Paracoccus haeundaesis

<220>
<223> crtI amino acid

<400> 12

Met Asn Ala His Ser Pro Ala Ala Lys Thr Ala Ile Val Ile Gly Ala
1 5 10 15

Gly Phe Gly Gly Leu Ala Leu Ala Ile Arg Leu Gln Ser Ala Gly Ile
20 25 30

Ala Thr Thr Leu Val Glu Ala Arg Asp Lys Pro Gly Gly Arg Ala Tyr
35 40 45

Val Trp His Asp Gln Gly His Val Phe Asp Ala Gly Pro Thr Val Ile
50 55 60

Thr Asp Pro Asp Ala Leu Lys Glu Leu Trp Ala Leu Thr Gly Gln Asp
65 70 75 80

Met Ala Arg Asp Val Thr Leu Met Pro Val Ser Pro Phe Tyr Arg Leu
85 90 95

Met Trp Pro Gly Gly Lys Val Phe Asp Tyr Val Asn Glu Ala Asp Gln
100 105 110

Leu Glu Arg Gln Ile Ala Gln Phe Asn Pro Asp Asp Leu Glu Gly Tyr
115 120 125

Arg Arg Phe Arg Asp Tyr Ala Glu Glu Val Tyr Gln Glu Gly Tyr Val
130 135 140

Lys Leu Gly Thr Val Pro Phe Leu Lys Leu Gly Gln Met Leu Lys Ala
145 150 155 160

Ala Pro Ala Leu Met Lys Leu Glu Ala Tyr Lys Ser Val His Ala Lys
165 170 175

Val Ala Thr Phe Ile Lys Asp Pro Tyr Leu Arg Gln Ala Phe Ser Tyr
180 185 190

His Thr Leu Leu Val Gly Gly Asn Pro Phe Ser Thr Ser Ser Ile Tyr
195 200 205

Ala Leu Ile His Ala Leu Glu Arg Arg Gly Gly Val Trp Phe Ala Lys
210 215 220

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Gly Gly Thr Asn Gln Leu Val Ala Gly Met Val Ala Leu Phe Glu Arg
225                 230                 235                 240

Leu Gly Gly Gln Met Met Leu Asn Ala Lys Val Ala Arg Ile Glu Thr
                245                 250                 255

Glu Gly Ala Arg Thr Thr Gly Val Thr Leu Ala Asp Gly Arg Ser Leu
            260                 265                 270

Arg Ala Asp Met Val Ala Ser Asn Gly Asp Val Met His Asn Tyr Arg
        275                 280                 285

Asp Leu Leu Gly His Thr Ala Arg Gly Gln Ser Arg Ala Lys Ser Leu
    290                 295                 300

Asp Arg Lys Arg Trp Ser Met Ser Leu Phe Val Leu His Phe Gly Leu
305                 310                 315                 320

Arg Glu Ala Pro Lys Asp Ile Ala His His Thr Ile Leu Phe Gly Pro
                325                 330                 335

Arg Tyr Arg Glu Leu Val Asn Glu Ile Phe Lys Gly Pro Lys Leu Ala
            340                 345                 350

Glu Asp Phe Ser Leu Tyr Leu His Ser Pro Cys Thr Thr Asp Pro Asp
        355                 360                 365

Met Ala Pro Pro Gly Met Ser Thr His Tyr Val Leu Ala Pro Val Pro
    370                 375                 380

His Leu Gly Arg Ala Glu Ile Asp Trp Ala Val Glu Gly Pro Arg Tyr
385                 390                 395                 400

Ala Asp Arg Ile Leu Ala Ser Leu Glu Glu Arg Leu Ile Pro Asn Leu
                405                 410                 415

Arg Ala Asn Leu Thr Thr Thr Arg Ile Phe Thr Pro Ala Asp Phe Ala
            420                 425                 430

Ser Glu Leu Asn Ala His His Gly Ser Ala Phe Ser Val Glu Pro Ile
        435                 440                 445

Leu Thr Gln Ser Ala Trp Phe Arg Pro His Asn Arg Asp Lys Thr Ile
    450                 455                 460

Arg Asn Phe Tyr Leu Val Gly Ala Gly Thr His Pro Gly Ala Gly Ile
465                 470                 475                 480

Pro Gly Val Val Gly Ser Ala Lys Ala Thr Ala Gln Val Met Leu Ser
                485                 490                 495

Asp Leu Ala Gly Ala
            500
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<210> 13
<211> 915
<212> DNA
<213> Paracoccus haeundaesis

<220>
<223> crtB gene

<400> 13
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acggcggcca agctgatgcc gccgggcatc cgcgacgaca cggtgatgct ctatgcctgg 120

tgccgccacg cggatgacgt gatcgacggt caggccctgg gcagccgccc cgaggcggtg 180

aacgacccgc aggcgcggct ggacggcctg cgcgtcgaca cgctggcggc cctgcagggc 240

gacggtccgg tgaccccgcc ctttgccgcg ctgcgcgcgg tggcgcggcg gcatgatttc 300

ccgcaggcct ggcccatgga cctgatcgaa ggcttcgcga tggatgtcga ggcgcgcgac 360

tatcgcacgc tggatgacgt gctggaatat tcctatcacg tcgcaggcat cgtcggcgtg 420

atgatggccc gcgtgatggg cgtgcgcgac gatcctgtcc tggaccgcgc ctgcgacctg 480

gggctggcgt tccagctgac caacatcgcg cgcgacgtga tcgacgatgc gcgcatcggg 540

cggtgctatc tgccggggga ctggctggac caggcgggcg cgcggatcga cgggccggtg 600

ccgtcgccgg agctgtacac agtgatcctc cggctgttgg atgaggcgga accctattac 660

gcgtcggcgc gggtgggtct ggcggatctg ccaccgcgct gcgcctggtc catcgccgcc 720

gcgctacgga tctatcgcgc catcgggctg cgcatccgca agagcgggcc gcaggcctat 780

cgccagcgga tcagcacgtc caaggctgcc aagatcggcc tgctgggcgt cgggggctgg 840

gatgtcgcgc gatcacgcct gccgggggcg ggcgtgtcgc ggcagggcct ctggacccgg 900

ccgcatcacg tctag 915

<210> 14
<211> 304
<212> PRT
<213> Paracoccus haeundaesis

<220>
<223> crtB amino acid

<400> 14
Met Ser Asp Leu Val Leu Thr Ser Thr Glu Ala Ile Thr Gln Gly Ser
1 5 10 15

Gln Ser Phe Ala Thr Ala Ala Lys Leu Met Pro Pro Gly Ile Arg Asp
20 25 30

Asp Thr Val Met Leu Tyr Ala Trp Cys Arg His Ala Asp Asp Val Ile
35 40 45

Asp Gly Gln Ala Leu Gly Ser Arg Pro Glu Ala Val Asn Asp Pro Gln
50 55 60

Ala Arg Leu Asp Gly Leu Arg Val Asp Thr Leu Ala Ala Leu Gln Gly
65 70 75 80

Asp Gly Pro Val Thr Pro Pro Phe Ala Ala Leu Arg Ala Val Ala Arg
85 90 95

Arg His Asp Phe Pro Gln Ala Trp Pro Met Asp Leu Ile Glu Gly Phe
100 105 110

Ala Met Asp Val Glu Ala Arg Asp Tyr Arg Thr Leu Asp Asp Val Leu
115 120 125

Glu Tyr Ser Tyr His Val Ala Gly Ile Val Gly Val Met Met Ala Arg
130 135 140

Val Met Gly Val Arg Asp Asp Pro Val Leu Asp Arg Ala Cys Asp Leu
145 150 155 160

Gly Leu Ala Phe Gln Leu Thr Asn Ile Ala Arg Asp Val Ile Asp Asp
165 170 175

Ala Arg Ile Gly Arg Cys Tyr Leu Pro Gly Asp Trp Leu Asp Gln Ala
180 185 190

Gly Ala Arg Ile Asp Gly Pro Val Pro Ser Pro Glu Leu Tyr Thr Val
195 200 205

Ile Leu Arg Leu Leu Asp Glu Ala Glu Pro Tyr Tyr Ala Ser Ala Arg
210 215 220

Val Gly Leu Ala Asp Leu Pro Pro Arg Cys Ala Trp Ser Ile Ala Ala
225 230 235 240

Ala Leu Arg Ile Tyr Arg Ala Ile Gly Leu Arg Ile Arg Lys Ser Gly
245 250 255

Pro Gln Ala Tyr Arg Gln Arg Ile Ser Thr Ser Lys Ala Ala Lys Ile
260 265 270

Gly Leu Leu Gly Val Gly Gly Trp Asp Val Ala Arg Ser Arg Leu Pro
275 280 285

Gly Ala Gly Val Ser Arg Gln Gly Leu Trp Thr Arg Pro His His Val
290 295 300

<210> 15
<211> 882
<212> DNA

<213> Paracoccus haeundaesis

<220>
<223> crtE gene

<400> 15
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gcccagggat tcggtgccgt gtcgcagccg ctcggcgcgg ccatgagcca tggcgcgctg 120

tcgtcgggca ggcggttccg cggcatgctg atgctgcttg cggcagaggc ctcgggcggg 180

gtctgcgaca cgatcgtcga cgccgcctgc gcggtcgaga tggtgcatgc cgcatcgctg 240

atcttcgacg acctgccctg catggacgat gccgggctgc gccgcggccg gcccgcgacc 300

catgtggcgc atggcgaaag ccgtgccgtg ctgggcggca tcgccctgat caccgaggca 360

atggccctgc tggccggtgc gcgcggcgcg tcgggcacgg tgcgggcgca gctggtgcgg 420

atcctgtcgc ggtccctggg gccgcagggc ctgtgcgccg gccaggacct ggacctgcac 480

gcggccaaga acggcgcggg ggtcgaacag gaacaggacc tgaagaccgg cgtgctgttc 540

atcgccgggc tggagatgct ggccgtgatc aaggagttcg acgccgagga gcagacccag 600

atgatcgact ttggccgtca gctgggccgc gtgttccagt cctatgacga cctgctggac 660

gtcgtgggcg accaggcggc gcttggcaag gataccggtc gcgatgccgc ggcccccggc 720

ccgcggcgcg gccttctggc cgtgtcagac ctgcagaacg tgtcccgtca ttacgaggcc 780

agccgcgccc aactggacgc gatgctgcgc agcaagcgcc ttcaggctcc ggaaatcgcg 840

gccctgctgg aacgggttct gccctacgcc gcgcgcgcct ag 882

<210> 16
<211> 293
<212> PRT
<213> Paracoccus haeundaesis

<220>
<223> crtE amino acid

<400> 16
Met Arg Arg Asp Val Asn Pro Ile His Ala Thr Leu Leu Gln Thr Arg
1 5 10 15

Leu Glu Glu Ile Ala Gln Gly Phe Gly Ala Val Ser Gln Pro Leu Gly
20 25 30

Ala Ala Met Ser His Gly Ala Leu Ser Ser Gly Arg Arg Phe Arg Gly
35 40 45

Met Leu Met Leu Leu Ala Ala Glu Ala Ser Gly Gly Val Cys Asp Thr
50 55 60

Ile Val Asp Ala Ala Cys Ala Val Glu Met Val His Ala Ala Ser Leu
65 70 75 80

Ile Phe Asp Asp Leu Pro Cys Met Asp Asp Ala Gly Leu Arg Arg Gly
85 90 95

Arg Pro Ala Thr His Val Ala His Gly Glu Ser Arg Ala Val Leu Gly
100 105 110

Gly Ile Ala Leu Ile Thr Glu Ala Met Ala Leu Leu Ala Gly Ala Arg
115 120 125

Gly Ala Ser Gly Thr Val Arg Ala Gln Leu Val Arg Ile Leu Ser Arg
130 135 140

Ser Leu Gly Pro Gln Gly Leu Cys Ala Gly Gln Asp Leu Asp Leu His
145 150 155 160

Ala Ala Lys Asn Gly Ala Gly Val Glu Gln Glu Gln Asp Leu Lys Thr
165 170 175

Gly Val Leu Phe Ile Ala Gly Leu Glu Met Leu Ala Val Ile Lys Glu
180 185 190

Phe Asp Ala Glu Glu Gln Thr Gln Met Ile Asp Phe Gly Arg Gln Leu
195 200 205

Gly Arg Val Phe Gln Ser Tyr Asp Asp Leu Leu Asp Val Val Gly Asp
210 215 220

Gln Ala Ala Leu Gly Lys Asp Thr Gly Arg Asp Ala Ala Ala Pro Gly
225 230 235 240

Pro Arg Arg Gly Leu Leu Ala Val Ser Asp Leu Gln Asn Val Ser Arg
245 250 255

His Tyr Glu Ala Ser Arg Ala Gln Leu Asp Ala Met Leu Arg Ser Lys
260 265 270

Arg Leu Gln Ala Pro Glu Ile Ala Ala Leu Leu Glu Arg Val Leu Pro
275 280 285

Tyr Ala Ala Arg Ala
290

<210> 17
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> forward primer for crt gene

<400> 17

gttccacgac tggggcatc 19

<210> 18
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> reverse primer for crt gene

<400> 18
tccactgacc ttgttggaca aattgccg 28